Amendments to the specification:

Replace paragraph [0021] (page 3, lines 22-26) with the following amended paragraph:

[0021] FIG. 6a illustrates an electrophoresis pattern in case cy3-pfM12 (5' cy3-AGA ACG CGC CTG 3') (SEQ ID NO: 4) which was obtained in Example 2 was used as a primer, and FIG. 6b illustrates an electrophoresis pattern in case FITC/UCS (5' FITC-CA GGA AAC AGC TAT GAC 3') (SEQ ID NO: 38) was used as a primer.

Replace paragraph [0030] (page 6, line 22, to page 8, line 6) with the following amended paragraph:

[0030] Apart from the normal PCR method, an appropriate sequence, length and kind of a primer can be appropriately selected for the random PCR. Experimentally and analytically the most simple system, however, is the case where a relatively short *single primer is used. Even in the case a single primer is* used, and a genome which is derived from the same microorganism is amplified, a kind and quantity of a double-stranded DNA fragment which can be amplified depend on the sequence and length of the primer. In addition even in the case a single primer and a primer which has the same sequence and length are used, a kind and quantity of a double-stranded DNA fragment which can be amplified depend on the microorganism from which the genome is derived. Considering these facts, sequence, length, and kind of a primer are appropriately selected. Too long primer can have the hair-pin structure, can

prevent annealing, and tends to lower a yield of a PCR product. Too short primer does not adequately stabilize a bonding containing mismatch (es), and tends to lower a yield of a PCR product. A length (base length) of a primer is suitably, for example, 8-20, preferably 10-16, more preferably 10-12, and most preferably 12. An oligonucleotide which has a length of 12 bases can be used as a primer. Such oligonucleotide primers include pfM4 (dCAGTCAGGACGT) (SEQ ID NO: 3), pfM12 (dAGAACGCGCCTG) (SEQ ID NO: 4), pfM14 (dCGTCGCTATTAA) (SEQ ID NO: 5), pfM19 (dCAGGGCGCGTAC) (SEQ ID NO: 6), $(dA)_{12}$ (dAAAAAAAAAAAA) (SEQ ID NO: 7), $(dA_3T_3)_2$ (dAAATTTAAATTT) (SEQ ID NO: 8), $(dAATT)_3$ (dAATTAATTAATT) (SEQ ID NO: 9), $(dACG)_4$ (dACGACGACGACG) (SEQ ID NO: 10), $(dAT)_6$ (dATATATATATAT) (SEQ ID NO: 11), $(dC)_{12}$ (dCCCCCCCCCCCC) (SEQ ID NO: 12), $(dCCGG)_3$ (dCCGGCCGGCCGG) (SEQ ID NO: 13), $(dG)_{12}$ (dGGGGGGGGGGGG) (SEQ ID NO: 15), $(dGA)_6$ (dGAGAGAGAGAGA) (SEQ ID NO: 16), $(dGGCC)_3$ (dGGCCGGCCGGCC) (SEQ ID NO: 17), (dCT)6 (dCTCTCTCTCTCT) (SEQ ID NO: 14), $(dT)_{12}$ (dTTTTTTTTTTTT) (SEQ ID NO: 18), $(dT_3G_3)_2$ (dTTTGGGTTTGGG) (SEQ ID NO: 19), $(dTGC)_4$ (dTGCTGCTGCTGC) (SEQ ID NO: 20), $(TA)_4C_2AC$ (dTATATATACCAC) (SEQ ID NO: 21), Colesive1 (dGGGCGGCGACCT) (SEQ ID NO: 22), Cohesive2 (dAGGTCGCCGCCC) (SEQ ID NO: 23), G4sand (dGGGGTCGAGGGG) (SEQ ID NO: 24), $GCTA_9$

(dGCTAAAAAAAAA) (SEQ ID NO: 25), notG (dCAATTCTACAAC) (SEQ ID NO: 26), notT (dACGAGCGAGCGC) (SEQ ID NO: 27), Promote1 (dTATAATTATAAT) (SEQ ID NO: 28), Promote2 (dATTATAATTATA) (SEQ ID NO: 29), SD1 (dGATCACCTCCTTA) (SEQ ID NO: 30), SD2 (dTAAGGAGGTGATC) (SEQ ID NO: 31), Telomere1 (dCCCACCCACCCA) (SEQ ID NO: 32), Telomere2 (dTGGGTGGGTGGG) (SEQ ID NO: 33), FITC17-H-3' (5' GAGGAAACAGCTATGAGATCT TCTC 3') (SEQ ID NO: 34), FITC17-H-5' (5' CAG GAA ACA GCT ATG ACG TTC TCA C 3') (SEQ ID NO: 35), LH-7-3' (5' GGC GAT ATC CCT GAA A 3') (SEQ ID NO: 36), LH-7-5' (5' TAT TAT TTC CGC AAA G 3') (SEQ ID NO: 37), M13 Reverse (5' CAG GAA ACA GCT ATG AC 3') (SEQ ID NO: 38), cy3-pfM12 (5' cy3-AGA ACG CGC CTG 3') (SEQ ID NO: 39) (with cy3 fluorescence), FITC/UCS (5' FITC-CA GGA AAC AGC TAT GAC 3') (SEQ ID NO: 40) (with FITC fluorescence), MA1-FITC (5' FITC-TGC TAC GTC TCT TCC GAT GCT GTC TTT CGC T 3') (SEQ ID NO: 41) (with FITC fluorescence), cy3-MA1 (5' cy3-TGC TAC GTC TCT TCC GAT GCT GTC TTT CGC T 3') (SEQ ID NO: 42) (with cy3 fluorescence), HEX-pfM11 (5' HEX-GAA CCT CCC GAC 3') (SEQ ID NO: 43) (with Hex fluorescence), TAM-TGC4 (5' TAM-TGC TGC TGC TGC 3') (SEQ ID NO: 44) (with Tamara fluorescence), and the like.

Replace paragraph [0102] (paragraph bridging pages 24 and 25) with the following amended paragraph:

[0102] One hundred μl of reaction mixture which contains 200 μM dNTP (N = G, A, T, C), 0.5 μM primer (pfM12 (dAGAACGCGCCTG) (SEQ ID NO: 39)), 10 mM Tris-HCl (pH 9.0), 50 mM KCl, 2.5 mM $MgCl_2$, 0.1% Triton X-100, 0.02 unit/μl Taq DNA polymerase, and an appropriate amount of template DNA (3 μl of a DNA solution was added, and the volume of the reaction mixture was adjusted to 100 μl) was prepared for each DNA. Double-stranded DNA fragments were prepared by PCR comprising the steps of 1) the treatment at 94 °C for 1 min, 2) 20-30 times repeating the cycle comprising denaturation at 94 °C. for 30 min, annealing at 28 °C. for 2 min, and elongation at 47 °C. for 2 min, followed by 3) the treatment at 47 °C. for 2 min.

Replace paragraph [0116] (page 27, lines 7-23) with the following amended paragraph:

[0116] Random PCR was carried out under the same condition except using DNA of Bacillus subtilis as a template, and cy3-pfM12 (5' cy3-AGA ACG CGC CTG 3') (SEQ ID NO: 4) which contains phosphor cy3 or FITC/UCS ~~(5' FITC-CAT GCA AAC AGC TAT GAC 3')~~ (5' FITC-CAGGAAACAG CTATGAC 3') (SEQ ID NO: 40) which contains phosphor FITC as a primer for each primer, and the obtained double-stranded amplified DNA fragments were mixed, and TGGE was carried out in a way which is similar to Example 1. An electrophoresis pattern by TGGE was

visualized with an excitation/fluorescent wavelength of 550 nm/570 nm (phosphor cy3) or 494 nm/519 nm (phosphor FITC). FIG. 6a illustrates an electrophoresis pattern in the case where cy3-pfM12 (5'cy3-AGA ACG CGC CTG 3') (SEQ ID NO: 4) was used as a primer, and FIG. 6b illustrates an electrophoresis pattern in the case where FITC/UCS ~~(5' FITC-CA GCA AAC AGC TAT GAC 3')~~ (5' FITC-CAGGAAACAG CTATGAC 3') (SEQ ID NO: 40) was used as a primer. Identification dots were extracted form each pattern. The microorganism which was used as a template was identified as Bacillus subtilis based the obtained identification dots.